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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/186,269A**DATE: 09/08/94  
TIME: 17:28:05*INPUT SET: S3560.raw*

**This Raw Listing contains the General  
Information Section and up to the first 5 pages.**

~~66~~  
**ENTERED**

1                   SEQUENCE LISTING  
2  
3       (1)      General Information:  
4  
5        (i)     APPLICANT: Bendig, Mary M.  
6                   Leger, Olivier J.  
7                   Saldanha, Jose  
8                   Jones, S. Tarran  
9  
10      (ii)    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
11                   Adhesion Molecule VLA-4  
12  
13      (iii)   NUMBER OF SEQUENCES: 45  
14  
15      (iv)    CORRESPONDENCE ADDRESS:  
16            (A) ADDRESSEE: Townsend and Townsend Khourie and Crew  
17            (B) STREET: One Market Plaza, Steuart Tower, Suite 2000  
18            (C) CITY: San Francisco  
19            (D) STATE: California  
20            (E) COUNTRY: USA  
21            (F) ZIP: 94105  
22  
23      (v)    COMPUTER READABLE FORM:  
24            (A) MEDIUM TYPE: Floppy disk  
25            (B) COMPUTER: IBM PC compatible  
26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
28  
29      (vi)   CURRENT APPLICATION DATA:  
30            (A) APPLICATION NUMBER: US 08/186,269  
31            (B) FILING DATE: 25-JAN-1994  
32            (C) CLASSIFICATION:  
33  
34      (viii)  ATTORNEY/AGENT INFORMATION:  
35            (A) NAME: Smith, William L.  
36            (B) REGISTRATION NUMBER: 30,223  
37            (C) REFERENCE/DOCKET NUMBER: 15270-14  
38  
39      (ix)   TELECOMMUNICATION INFORMATION:  
40            (A) TELEPHONE: 415-543-9600  
41            (B) TELEFAX: 415-543-5043  
42  
43  
44      (2)   INFORMATION FOR SEQ ID NO:1:  
45  
46        (i)   SEQUENCE CHARACTERISTICS:

**RAW SEQUENCE LISTING  
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47 (A) LENGTH: 483 base pairs  
 48 (B) TYPE: nucleic acid  
 49 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

51  
 52 (ii) MOLECULE TYPE: cDNA  
 53

54  
 55 (ix) FEATURE:  
 56 (A) NAME/KEY: CDS  
 57 (B) LOCATION: 53..430  
 58

59  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

62 ATGAGGGCCC CTGCTCAGAT TTTTGGATT TTGGTCAGGA GACGTTGTAG AA ATG	55
63	Met
64	1
65	
66 AGA CCG TCT ATT CAG TTC CTG GGG CTC TTG TTG TTC TGG CTT CAT GGT	103
67 Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Phe Trp Leu His Gly	
68 5 10 15	
69	
70 GCT CAG TGT GAC ATC CAG ATG ACA CAG TCT CCA TCC TCA CTG TCT GCA	151
71 Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
72 20 25 30	
73	
74 TCT CTG GGA GGC AAA GTC ACC ATC ACT TGC AAG ACA AGC CAA GAC ATT	199
75 Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp Ile	
76 35 40 45	
77	
78 AAC AAG TAT ATG GCT TGG TAC CAA CAC AAG CCT GGA AAA CGT CCT AGG	247
79 Asn Lys Tyr Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro Arg	
80 50 55 60 65	
81	
82 CTG CTC ATA CAT TAC ACA TCT GCA TTA CAG CCA GGC ATC CCA TCA AGG	295
83 Leu Leu Ile His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser Arg	
84 70 75 80	
85	
86 TTC AGT GGA AGT GGG TCT GGG AGA GAT TAT TCC TTC AAC ATC AGC AAC	343
87 Phe Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser Asn	
88 85 90 95	
89	
90 CTG GAG CCT GAA GAT ATT GCA ACT TAT TAT TGT CTA CAG TAT GAT AAT	391
91 Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn	
92 100 105 110	
93	
94 CTG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGGGCTGATG	440
95 Leu Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	
96 115 120 125	
97	
98 CTGCACCAAC TGTATCCATC TTCCCCACCAT CCACCCGGGA TCC	483
99	

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/186,269A**DATE: 09/08/94  
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100 (2) INFORMATION FOR SEQ ID NO:2:

101

102 (i) SEQUENCE CHARACTERISTICS:  
103 (A) LENGTH: 126 amino acids  
104 (B) TYPE: amino acid  
105 (D) TOPOLOGY: linear

106

107 (ii) MOLECULE TYPE: protein

108

109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

110

111 Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His  
112 1 5 10 15

113

114 Gly Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
115 20 25 30

116

117 Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp  
118 35 40 45

119

120 Ile Asn Lys Tyr Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro  
121 50 55 60

122

123 Arg Leu Leu Ile His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser  
124 65 70 75 80

125

126 Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser  
127 85 90 95

128

129 Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp  
130 100 105 110

131

132 Asn Leu Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
133 115 120 125

134

135

136 (2) INFORMATION FOR SEQ ID NO:3:

137

138 (i) SEQUENCE CHARACTERISTICS:  
139 (A) LENGTH: 470 base pairs  
140 (B) TYPE: nucleic acid  
141 (C) STRANDEDNESS: double  
142 (D) TOPOLOGY: linear

143

144 (ii) MOLECULE TYPE: cDNA

145

146

147 (ix) FEATURE:  
148 (A) NAME/KEY: CDS  
149 (B) LOCATION: 1..420

150

151

152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

**RAW SEQUENCE LISTING  
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153				
154	ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG			48
155	Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly			
156	1	5	10	15
157				
158	GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG			96
159	Val Asn Ser Glu Val Gln Leu Gln Ser Gly Ala Glu Leu Val Lys			
160	20	25	30	
161				
162	CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT			144
163	Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile			
164	35	40	45	
165				
166	AAA GAC ACC TAT ATA CAC TGT GTG AAG CAG AGG CCT GAA CAG GGC CTG			192
167	Lys Asp Thr Tyr Ile His Cys Val Lys Gln Arg Pro Glu Gln Gly Leu			
168	50	55	60	
169				
170	GAG TGG ATT GGA AGG ATT GAT CCT GCG AAT GGT TAT ACT AAA TAT GAC			240
171	Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Tyr Thr Lys Tyr Asp			
172	65	70	75	80
173				
174	CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCT GAC ACA TCC TCC AAC			288
175	Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn			
176	85	90	95	
177				
178	ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC			336
179	Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val			
180	100	105	110	
181				
182	TAT TTC TGT GCT AGA GAG GGA TAT TAT GGT AAC TAC GGG GTC TAT GCT			384
183	Tyr Phe Cys Ala Arg Glu Gly Tyr Tyr Gly Asn Tyr Gly Val Tyr Ala			
184	115	120	125	
185				
186	ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCCTCAGCCA			430
187	Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val			
188	130	135	140	
189				
190	AAACGACACC CCCATCTGTC TATCCACTGG CCCGGGATCC			470
191				
192				
193	(2) INFORMATION FOR SEQ ID NO:4:			
194				
195	(i) SEQUENCE CHARACTERISTICS:			
196	(A) LENGTH: 140 amino acids			
197	(B) TYPE: amino acid			
198	(D) TOPOLOGY: linear			
199				
200	(ii) MOLECULE TYPE: protein			
201				
202	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:			
203				
204	Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly			
205	1	5	10	15

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206  
207 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys  
208 20 25 30  
209  
210 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile  
211 35 40 45  
212  
213 Lys Asp Thr Tyr Ile His Cys Val Lys Gln Arg Pro Glu Gln Gly Leu  
214 50 55 60  
215  
216 Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Tyr Thr Lys Tyr Asp  
217 65 70 75 80  
218  
219 Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn  
220 85 90 95  
221  
222 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
223 100 105 110  
224  
225 Tyr Phe Cys Ala Arg Glu Gly Tyr Tyr Gly Asn Tyr Gly Val Tyr Ala  
226 115 120 125  
227  
228 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val  
229 130 135 140  
230  
231 (2) INFORMATION FOR SEQ ID NO:5:  
232  
233 (i) SEQUENCE CHARACTERISTICS:  
234 (A) LENGTH: 106 amino acids  
235 (B) TYPE: amino acid  
236 (C) STRANDEDNESS: single  
237 (D) TOPOLOGY: linear  
238  
239 (ii) MOLECULE TYPE: protein  
240  
241  
242  
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
244  
245 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
246 1 5 10 15  
247  
248 Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp Ile Asn Lys Tyr  
249 20 25 30  
250  
251 Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro Arg Leu Leu Ile  
252 35 40 45  
253  
254 His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly  
255 50 55 60  
256  
257 Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser Asn Leu Glu Pro  
258 65 70 75 80

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**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/08/186,269A**

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Original Text